

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 6, 2004, 19:24:00 ; Search time 120.375 Seconds  
(without alignments)  
43.019 Million cell updates/sec

Title: US-10-618-644-4  
Perfect score: 58  
Sequence: 1 IPPGVVWY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	517	2	Q7GC77 glycine max
2	58	100.0	517	2	Q39922 glycine soj
3	58	100.0	517	2	Q8SB12 glycine max
4	58	100.0	560	2	Q8S900 glycine max
5	58	100.0	562	2	Q43452 glycine max
6	58	100.0	563	2	Q39921 glycine soj
7	58	100.0	563	2	Q9SB11 glycine max
8	57	98.3	136	2	Q43672 vicia faba
9	57	98.3	564	2	Q43673 vicia faba
10	57	98.3	566	2	Q4294 pium sativ
11	56	96.6	536	2	Q9FEC5 glycine max
12	56	96.6	536	2	Q6DR94 glycine max
13	52	89.7	562	1	GLC4 SOYBN
14	49	84.5	308	2	Q43671 vicia faba
15	49	84.5	484	1	LSG4 VICFA
16	49	84.5	485	2	Q41703 vicia sativ
17	49	84.5	503	1	LEGJ_PEA
18	48	82.8	516	1	GLC5 SOYBN
19	48	82.8	517	2	Q93707 glycine max
20	48	82.8	517	2	Q93708 glycine max
21	46	79.3	363	2	Q82427 oryza sativ
22	44	75.9	165	2	Q8P9R4 xanthomonas
23	44	75.9	427	2	Q8PLJ6 xanthomonas
24	43	74.1	168	2	Q94704 schizosacch
25	43	74.1	183	2	Q6TM56 bacterioph
26	43	74.1	183	2	Aac94484 bacterioph
27	43	74.1	707	2	Q9F348 streptomyc
28	42	72.4	242	2	Q46604 sus scrofa
29	42	72.4	323	2	Q9NUJ7 homo sapien
30	42	72.4	330	2	Q63241 rattus norv
31	42	72.4	331	2	Q63239 rattus norv

32	42	72.4	503	1	NORB_CHLCV	Q823p2 chlamydomphi
33	42	72.4	503	1	NORB_CHLMU	Q9pbk6 chlamydia m
34	42	72.4	503	1	NORB_CHLPN	Q9zbb6 chlamydia p
35	42	72.4	503	1	NORB_CHLTR	Q84280 chlamydia t
36	42	72.4	509	2	Q6MEH4	Q6meh4 parachlamyd
37	42	72.4	509	2	CAF23025	CAF23025 parachlam
38	42	72.4	555	2	Q9VHV2	Q9vkv2 drosophila
39	42	72.4	568	2	Q8GNZ3	Q8gnz3 drosophila
40	42	72.4	705	2	Q63710	Q63710 rattus ratt
41	42	72.4	707	2	Q9TT07	Q9tt07 canis famill
42	42	72.4	723	2	Q86VI4	Q86vi4 homo sapien
43	41.5	71.6	548	2	Q9F3U5	Q9f3u5 pseudomonas
44	41.5	71.6	561	2	Q91UN3	Q91un3 plasmid psb
45	41.5	71.6	569	2	O08449	O08449 pseudomonas

ALIGNMENTS

RESULT 1  
Q7GC77 PRELIMINARY; PRT; 517 AA.  
AC Q7GC77; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Glycinin A3B4 subunit.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cotyledon;  
RA Adachi M., Katsube T., Masuda T., Utsuni S.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
CC -I- SUBUNIT: Hexamer; each subunit is composed of an acidic and a  
CC basic chain derived from a single precursor and linked by a  
CC disulfide bond (By similarity)  
CC -I- SIMILARITY: Belongs to the 11S seed storage protein (globulins)  
CC family.  
DR EMBL; AB049440; BAB15802.1; -.  
DR InterPro; IPR006045; Cupin.  
DR InterPro; IPR007113; Cupin region.  
DR InterPro; IPR011051; RmlC like cupin.  
DR InterPro; IPR006044; Seedstore\_11s.  
DR Pfam; PF00190; Cupin; 2.  
DR PRINTS; PR00439; 11SGLOBULIN.  
DR PROSITE; PS00305; 11S\_SEED\_STORAGE; 1.  
KW Seed storage protein; Storage protein.  
SQ SEQUENCE 517 AA; 58187 MW; 0440F4C72181B7C CRC64;

Query Match 100.0%; Score 58; DB 2; Length 517;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPPGVVWY 9  
Db 149 IPPGVVWY 157

RESULT 2

Q39922 PRELIMINARY; PRT; 517 AA.  
ID Q39922  
AC Q39922;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE G5 protein.  
GN Name=G5;  
OS Glycine soja (Wild soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DR PROSITE; PS00305; 11S SEED STORAGE; 1.
KW Seed storage protein; Storage protein.
SQ SEQUENCE 517 AA; 58229 MW; 0E1F51BC72181B7C CRC64;

Query Match 100.0%; Score 58; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPPGVPTWT 9
Db 149 IPPGVPTWT 157

RESULT 4
Q9S9D0 PRELIMINARY; PRT; 560 AA.
AC Q9S9D0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glycinin G4 subunit.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92393391; PubMed=2485233;
RX Nielsen N.C., Dickinson C.D., Cho T.J., Thanh V.H., Scallan B.J.,
RA Fischer R.L., Sims T.L., Drews G.N., Goldberg R.B.;
RT "Characterization of the glycinin gene family in soybean.";
RL Plant Cell 1:313-328(1989).
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond (By similarity).
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
DR PIR; S11004; S11004.
DR HSP; P04776; 1PXZ.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR011051; RmlC_like_cupin.
DR InterPro; IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR PROSITE; PS00305; 11S SEED STORAGE; 1.
DR PROSITE; PS00305; 11S SEED STORAGE; 1.
SQ SEQUENCE 560 AA; 63679 MW; F95DBEA4012DA024 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPPGVPTWT 9
Db 149 IPPGVPTWT 157

RESULT 5
Q43452 PRELIMINARY; PRT; 562 AA.
ID Q43452
AC Q43452;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycinin precursor.
DE Name=Gy4;
GN Glycine max (Soybean)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]

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RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RX MEDLINE=92256811; PubMed=1316192;  
RA Rue Z.T., Xu M.L., Shen W., Zhuang N.L., Hu W.M., Shen S.C.;  
RT "Characterization of the Gy4 Glycine gene from soybean Glycine max cv.  
RL Plant Mol. Biol. 18:897-908(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Rue Z.T.;  
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a  
CC basic chain derived from a single precursor and linked by a  
CC disulfide bond (By similarity).  
CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)  
CC family.  
DR EMBL; X52863; CAA37044.1; -.  
DR PIR; P00199; P00199.  
DR PIR; S20946; S20946.  
DR HSP; P04776; IFXZ.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR006045; Cupin.  
DR InterPro; IPR011051; RmlC like\_cupin.  
DR InterPro; IPR006044; Seedstore\_11s.  
DR Pfam; PF00190; Cupin; 2.  
DR PRINTS; PR00439; 11SGLOBULIN.  
DR PROSITE; PS00305; IIS\_SEED\_STORAGE; 1.  
KW Signal.  
FT CHAIN 1 23 Potential.  
FT CHAIN 24 562 Glycinin.  
FT CHAIN 562 AA; 63876 MW; 3A4EF28B448AB15A CRC64;  
SQ SEQUENCE 562 AA; 63876 MW; 3A4EF28B448AB15A CRC64;  
Query Match 100.0%; Score 58; DB 2; Length 562;  
Best Local Similarity 100.0%; Pred. No. 0.77;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IPPGVPTWT 9  
Db 148 IPPGVPTWT 156  
RESULT 6  
ID Q39921 PRELIMINARY; PRT; 563 AA.  
AC Q39921;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE AS4B3 subunit.  
GN Name=glycinin Gy4;  
OS Glycine soja (Wild soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3848;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SH1;  
RA Rue Z.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a  
CC basic chain derived from a single precursor and linked by a  
CC disulfide bond (By similarity).  
CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)  
CC family.  
DR EMBL; X86570; CAA60533.1; -.  
DR PIR; S54802; S54802.  
DR HSP; P04776; IFXZ.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR006045; Cupin.  
DR InterPro; IPR011051; RmlC like\_cupin.  
DR InterPro; IPR006044; Seedstore\_11s.

DR Pfam; PF00190; Cupin; 2.  
DR PRINTS; PR00439; 11SGLOBULIN.  
DR PROSITE; PS00305; IIS\_SEED\_STORAGE; 1.  
SQ SEQUENCE 563 AA; 63806 MW; EC171BED5F2B361F CRC64;  
Query Match 100.0%; Score 58; DB 2; Length 563;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IPPGVPTWT 9  
Db 149 IPPGVPTWT 157  
RESULT 7  
ID Q9SB11 PRELIMINARY; PRT; 563 AA.  
AC Q9SB11;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Glycinin.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaves;  
RA Chen S., Arahira M., Fukazawa C.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a  
CC basic chain derived from a single precursor and linked by a  
CC disulfide bond (By similarity).  
CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)  
CC family.  
DR EMBL; AB004062; BAA74953.1; -.  
DR PIR; P00199; P00199.  
DR HSP; P04776; IFXZ.  
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.  
DR InterPro; IPR006045; Cupin.  
DR InterPro; IPR011051; RmlC like\_cupin.  
DR InterPro; IPR006044; Seedstore\_11s.  
DR Pfam; PF00190; Cupin; 2.  
DR PRINTS; PR00439; 11SGLOBULIN.  
DR PROSITE; PS00305; IIS\_SEED\_STORAGE; 1.  
SQ SEQUENCE 563 AA; 63797 MW; 4ACC765C55AB9E18 CRC64;  
Query Match 100.0%; Score 58; DB 2; Length 563;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IPPGVPTWT 9  
Db 149 IPPGVPTWT 157  
RESULT 8  
ID Q43672 PRELIMINARY; PRT; 136 AA.  
AC Q43672;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Legumin; legumin-related high molecular weight polypeptide  
DE (Fragment).  
GN Name=LelB161;  
OS Vicia faba (Broad bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
OX NCBI\_TaxID=3906;

KW	FT	SQ
Seed storage protein; Signal; Storage protein.	Seed storage protein; Signal; Storage protein.	Seed storage protein; Signal; Storage protein.
SIGNAL	SIGNAL	SIGNAL
SEQUENCE	SEQUENCE	SEQUENCE
564 AA;	564 AA;	564 AA;
64502 MW;	64502 MW;	64502 MW;
568E497245A1915A CRC64;	568E497245A1915A CRC64;	568E497245A1915A CRC64;

AC	Q9FEC5; 2001	(TrEMBLrel. 16, Created)
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)
DI	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)
DE	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE	Glycinin subunit G7.	

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GN Name=GY7;
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Beilinson V., Chen Z., Shoemaker R.C., Fischer R.L., Goldberg R.B.,
RA Nielsen N.C.;
RT "Genomic organization of glycinin genes in soybean.";
RL EMBL: AF319777; AAG42489.1; -.
DR EMBL: AF319776; AAG42488.1; -.
DR HSP; P04776; IPXZ.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR007113; Cupin_region.
DR InterPro; IPR011051; RmlC_like_cupin.
DR InterPro; IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR SEQUENCE 536 AA; 60486 MW; 40F452FAA067FBC7 CRC64;

Query Match 96.6%; Score 56; DB 2; Length 536;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPFGVPYWT 9
DB 137 VPPGIPYWT 145

RESULT 12
Q6DR94
ID Q6DR94 PRELIMINARY; PRT; 536 AA.
AC Q6DR94
DT 01-OCT-2004 (T-EMBLrel. 28, Created)
DT 01-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Glycinin subunit G7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Mi D., Li J.Y., Zhang W.;
RC TISSUE=Leaf;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY649099; AAT68239.1; -.
DR SEQUENCE 536 AA; 60514 MW; 94EF37198D1C4468 CRC64;

Query Match 96.6%; Score 56; DB 2; Length 536;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPFGVPYWT 9
DB 137 VPPGIPYWT 145

RESULT 13
GLC4 SOYBN
ID GLC4 SOYBN STANDARD; PRT; 562 AA.
AC P02858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4 subunit; Glycinin B3 subunit].
GN Name=GY4;

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OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Boninori;
RX MEDLINE=85330642; PubMed=2988947;
RA Momma T., Negro T., Hirano H., Uchimoto A., Uchimoto K., Fukazawa C.;
RT "Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a
RT splitting storage protein subunit of soybean.";
RL Eur. J. Biochem. 149:491-496(1985).
RN [2]
RP SEQUENCE (A4/A5 SUBUNITS).
RA STRAIN=cv. Boninori;
RA Hirano H., Fukazawa C., Harada K.;
RT "The primary structures of the A4 and A5 subunits are highly
RT homologous to that of the A3 subunit in the glycinin seed storage
RT protein of soybean.";
RN FEBS Lett. 181:124-128(1985).
RN [3]
RP SEQUENCE OF 181-386 FROM N.A.
RA STRAIN=cv. CX635-1-1-1;
RA Scallan B.J., Dickinson C.D., Nielsen N.C.;
RT "Characterization of a null-allele for the G4 glycinin gene from
RT soybean.";
RL Mol. Gen. Genet. 208:107-113(1987).
CC -!- FUNCTION: Glycinin is the major seed storage protein of soybean.
CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond.
CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02626; CAA26478.1; -.
CC EMBL; X05652; CAB57802.1; -.
CC PIR; A91145; FWSYGS.
CC HSP; P04776; IPXZ.
CC InterPro; IPR006045; Cupin.
CC InterPro; IPR011051; RmlC_like_cupin.
CC InterPro; IPR006044; Seedstore_11s.
CC Pfam; PF00190; Cupin; 2.
CC PRINTS; PR00439; 11SGLOBULIN.
CC PROSITE; PS00305; 11S_SEED_STORAGE; 1.
KW Direct protein sequencing; Multigene family; Seed storage protein;
KW Signal.
FT SIGNAL 1
FT CHAIN 23
FT CHAIN 24 120 Glycinin A5 subunit.
FT CHAIN 121 377 Glycinin A4 subunit.
FT CHAIN 378 562 Glycinin B3 subunit.
FT DISULFID 108 384 Interchain (By similarity).
FT CONFLICT 29 29 L -> F (in Ref. 2).
FT CONFLICT 82 82 S -> L (in Ref. 2).
FT CONFLICT 86 86 S -> L (in Ref. 2).
FT CONFLICT 94 94 I -> V (in Ref. 2).
FT CONFLICT 101 103 LGV -> IGM (in Ref. 2).
FT CONFLICT 105 105 I -> F (in Ref. 2).
FT CONFLICT 117 117 E -> Q (in Ref. 2).
FT CONFLICT 253 253 E -> Q (in Ref. 3).
FT CONFLICT 332 335 NKTG -> EODQD (in Ref. 3).
SQ SEQUENCE 562 AA; 63587 MW; F5A06B8856B9BBD6 CRC64;

Query Match 89.7%; Score 52; DB 1; Length 562;
Best Local Similarity 88.9%; Pred. No. 7;

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Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	IPPGVPYWT 9							
Db	149	IPPSVPYWT 157							
RESULT 14									
Q43671		PRELIMINARY;	PRT;	308 AA.					
AC	Q43671;								
DT	01-NOV-1996	(TrEMBLrel. 01, Created)							
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)							
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)							
DE	Storage protein.								
OS	Vicia faba (Broad bean).								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;								
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.								
OX	NCBI_TaxID=3906;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Leaf;								
RX	MEDLINE=91370849; PubMed=2491681;								
RA	Heim U., Schubert R., Baumlein H., Wobus U.;								
RT	"The legumin gene family: structure and evolutionary implications of								
RL	Vicia faba B-type genes and pseudogenes.";								
RL	Plant Mol. Biol. 13:653-663(1989).								
DR	EMBL; X14238; CAA32455.1; -.								
DR	HSSP; P04776; lFXZ.								
GO	GO:0045735; F.nutrient reservoir activity; IEA.								
DR	InterPro; IPR006045; Cupin.								
DR	InterPro; IPR007113; Cupin_region.								
DR	InterPro; IPR011051; RmlC like_cupin.								
DR	Pfam; PF00190; Cupin; 2.								
DR	PRINTS; PR00439; lISGLOBULIN.								
SQ	SEQUENCE 308 AA; 34233 MW; E6CD2B1B1D063B99 CRC64;								
Query Match	84.5%;	Score 49;	DB 2;	Length 308;					
Best Local Similarity	77.8%;	Pred. No. 11;							
Matches	7;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	IPPGVPYWT 9							
Db	147	IPSGIPYWT 155							
RESULT 15									
LEG4_VICFA		STANDARD;	PRT;	484 AA.					
ID	LEG4_VICFA								
AC	P05130;								
DT	13-AUG-1987	(Rel. 05, Created)							
DT	13-AUG-1987	(Rel. 05, Last sequence update)							
DT	05-JUL-2004	(Rel. 44, Last annotation update)							
DE	Legumin type B precursor [Contains: Legumin type B alpha chain								
DE	(legumin type B acidic chain); Legumin type B beta chain (legumin type								
DE	B basic chain)].								
GN	Names=LEB4;								
OS	Vicia faba (Broad bean).								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;								
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.								
OX	NCBI_TaxID=3906;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=86176760; PubMed=3960730;								
RA	Baumlein H., Wobus U., Pustell J., Kafatos F.C.;								
RT	"The legumin gene family: structure of a B type gene of Vicia faba and								
RT	a possible legumin gene specific regulatory element.";								
RL	Nucleic Acids Res. 14:2707-2720(1986).								
CC	- - FUNCTION: This protein found in the seeds of many leguminous and								
CC	nonleguminous plants is the source of sulfur-containing amino								

acids in seed meals.

-|- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond.

-|- SIMILARITY: Belongs to the l1s seed storage protein (globulins) family.

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EMBL; X03677; CAA27313.1; -.

HSSP; P04776; lFXZ.

InterPro; IPR006045; Cupin.

InterPro; IPR007113; Cupin\_region.

InterPro; IPR011051; RmlC like\_cupin.

InterPro; IPR006044; Seedstore\_l1s.

Pfam; PF00190; Cupin; 2.

PRINTS; PR00439; lISGLOBULIN.

PROSITE; PS00305; l1s SEED STORAGE; 1.

Multigene family: Seed storage protein; Signal.

SIGNAL 1 22 Potential.

CHAIN 23 303 Legumin type B alpha chain.

CHAIN 304 484 Legumin type B beta chain.

DISULFID 109 310 Interchain (alpha-beta) (Potential).

DOMAIN 111 134 Gln-rich.

DOMAIN 194 230 Gln/Glu-rich.

DOMAIN 284 302 Gln/Glu-rich.

SEQUENCE 484 AA; 54447 MW; 3A40F53F43F3D737 CRC64;

Query Match 84.5%; Score 49; DB 1; Length 484;

Best Local Similarity 77.8%; Pred. No. 18;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPYWT 9

Db 147 IPSGIPYWT 155

Search completed: November 6, 2004, 19:52:53

Job time : 122.375 secs